

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 66 Seconds  
(without alignments)  
169.108 Million cell updates/sec

Title: US-09-824-134-2\_COPY\_130\_245  
Perfect score: 593  
Sequence: 1 FEAGAAAGAAPEEDLCAAF.....QEVQQAQDLQNRSGAMSPMS 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593	100.0	208	A56912	FADD protein - hum
2	115.5	19.5	656	I49299	receptor interacti
3	114.5	19.3	1856	B35049	ankyrin 1, erythro
4	114.5	19.3	1880	A35049	ankyrin 1, erythro
5	114.5	19.3	1881	SJHUK	ankyrin 1, erythro
6	112.5	19.0	1848	S37771	ankyrin, erythrocy
7	112.5	19.0	1862	I49502	ankyrin - mouse
8	111.5	18.8	671	T09479	serine/threonine p
9	103	17.4	2039	T15347	ankyrin-related un
10	96.5	16.3	3924	S37431	ankyrin 2, neuro
11	93	15.7	324	JC2395	Fas antigen precu
12	86	14.5	1765	T42714	ankyrin 3, splice
13	86	14.5	1940	T42715	ankyrin 3, splice
14	86	14.5	1943	T42713	ankyrin 3, splice
15	86	14.5	1957	T45627	myosin heavy chain
16	86	14.5	1961	T42716	ankyrin 3, splice
17	86	14.5	4377	A55575	ankyrin 3, long sp
18	84	14.2	138	S37773	ankyrin, erythrocy
19	84	14.2	1955	T30934	myosin-like protei
20	83	14.0	657	A53545	protein p84 - huma
21	81	13.7	312	A56911	TRADD protein - hu
22	79.5	13.4	724	A38749	3-phosphatidylinos
23	76.5	12.9	374	H75002	methyl-accepting c
24	75.5	12.7	549	B86264	hypothetical prote
25	75	12.6	313	MXRBR	nonstructural prot
26	74.5	12.6	455	GQHUT1	tumor necrosis fac
27	74	12.5	427	1 GQHUN	nerve growth facto
28	74	12.5	433	A32992	cyclin B1 - human
29	73.5	12.4	2325	T15566	hypothetical prote

RESULT 1

A56912  
FADD protein - human  
N:Alternate names: FAS-associating death domain containing protein FADD; mediator of re  
C:Species: Homo sapiens (man)  
C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: A56912; I38041  
R:Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.  
Cell 81, 503-512, 1995  
A:Title: FADD, a novel death domain-containing protein, interacts with the death domain  
A:Reference number: A56912; MUID:95277837; PMID:7538907  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-208 <CHI>  
A:Cross-references: UNIPROT:Q13158; GB:U24231; NID:G809486; PIDN:AAA86517.1; PID:G80948  
R:Boldin, M.P.; Vafolomeev, E.E.; Pancer, Z.; Malt, I.L.; Camonis, J.H.; Wallach, D.  
J. Biol. Chem. 270, 7795-7798, 1995  
A:Title: A novel protein that interacts with the death domain of Fas/APO1 contains a se  
A:Reference number: I38041; MUID:95229578; PMID:7536190  
A:Accession: I38041  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-31,'V',33-208 <RES>  
A:Cross-references: EMBL:X84709; NID:G791037; PIDN:CAA59197.1; PID:G791038  
C:Genetics:  
A:Gene: GDB:FADD; MORT1  
A:Cross-references: GDB:1320394  
C:Superfamily: receptor-induced toxicity mediator MORT1  
C:Keywords: apoptosis

Query Match 100.0%; Score 593; DB 2; Length 208;

Best Local Similarity 100.0%; Pred. No. 5.3e-49; Indels 0; Gaps 0;  
Matches 116; Conservative 0; Mismatches 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICDVGKDWRLARQLKVSPTKIDSIEDRYPRNLTERV 60  
|||||  
Db 82 FEAGAAAGAAPEEDLCAAFNVICDVGKDWRLARQLKVSPTKIDSIEDRYPRNLTERV 141  
|||||  
QY 61 RESLRWKTKENATVAHLVGLRSCQNLVADLVQEVQQAQDLQNRSGAMSPMS 116  
|||||  
Db 142 RESLRWKTKENATVAHLVGLRSCQNLVADLVQEVQQAQDLQNRSGAMSPMS 197  
|||||

RESULT 2

I49299  
receptor interacting protein RIP - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: I49299  
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995



RESULT 5  
SJHUK

ankyrin 1, erythrocyte splice form 1 - human  
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N;Contains: ankyrin 2.2  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S08275; A33219; PC22220; A35443  
R;Lux, S.E.; John, K.M.; Bennett, V.  
Nature 344, 36-42, 1990  
A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure  
A;Reference number: S08275; MUID:90158830; PMID:2137557  
A;Accession: S08275  
A;Molecule type: mRNA  
A;Residues: 1-1881 <LUJ>  
A;Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702  
A;Accession: A33219  
A;Molecule type: protein  
A;Residues: 2-7,'X',9-17,'X',19-20,'T',22-30;733-749,'A',751-753;828-833,'X',835-855,'X'  
X',1367;1383-1427;1601-1630;1686-1698,'D',1700;1763-1772 <LUX>  
A;Note: 845-Arg and 1392-Thr were also found  
R;Hermann, J.; Barel, M.; Prade, R.  
Biochem. Biophys. Res. Commun. 204, 453-460, 1994  
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane  
A;Reference number: PC2220; MUID:95071348; PMID:7526850  
A;Accession: PC2220  
A;Molecule type: protein  
A;Residues: 910-929 <HER>  
R;Davis, L.H.; Bennett, V.  
J. Biol. Chem. 265, 10589-10596, 1990  
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger  
A;Reference number: A35443; MUID:90285190; PMID:2141335  
A;Accession: A35443  
A;Molecule type: protein  
A;Residues: 'X',5,'X',7-12;403-417,'X',419-422,'H',424,'LQ';797-800,'L',802-814;862-863,  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing; phosphoprotein  
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>  
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>  
F;2-827/Region: anion exchange predicted <DOM1>  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>  
F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>  
F;828-1382/Domain: 62K #status predicted <DOM2>  
F;1383-1881/Region: spectrin binding  
F;1383-1881/Region: 55K #status predicted <DOM3>

R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  
Mamm. Genome 3, 281-285, 1992  
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain  
A;Reference number: 149502; MUID:92345717; PMID:1386265  
A;Accession: I49502  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1862 <RES>  
A;Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940  
C;Genetics:  
A;Gene: Ank-1  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;40-72/Domain: ankyrin repeat homology <AN01>  
F;73-105/Domain: ankyrin repeat homology <AN02>  
F;106-138/Domain: ankyrin repeat homology <AN03>  
F;139-167/Domain: ankyrin repeat homology <AN04>  
F;168-200/Domain: ankyrin repeat homology <AN05>  
F;201-233/Domain: ankyrin repeat homology <AN06>  
F;234-266/Domain: ankyrin repeat homology <AN07>  
F;267-299/Domain: ankyrin repeat homology <AN08>  
F;300-332/Domain: ankyrin repeat homology <AN09>  
F;333-365/Domain: ankyrin repeat homology <AN10>  
F;366-398/Domain: ankyrin repeat homology <AN11>  
F;399-431/Domain: ankyrin repeat homology <AN12>  
F;432-464/Domain: ankyrin repeat homology <AN13>  
F;465-497/Domain: ankyrin repeat homology <AN14>  
F;498-530/Domain: ankyrin repeat homology <AN15>  
F;531-563/Domain: ankyrin repeat homology <AN16>  
F;564-596/Domain: ankyrin repeat homology <AN17>  
F;597-629/Domain: ankyrin repeat homology <AN18>  
F;630-662/Domain: ankyrin repeat homology <AN19>  
F;663-695/Domain: ankyrin repeat homology <AN20>  
F;696-728/Domain: ankyrin repeat homology <AN21>  
F;729-761/Domain: ankyrin repeat homology <AN22>  
F;762-794/Domain: ankyrin repeat homology <AN23>  
Query Match 19.08; Score 112.5; DB 2; Length 1862;  
Best Local Similarity 29.08; Pred. No. 0.024;  
Matches 29; Conservative 27; Mismatches 37; Indels 7; Gaps 2;  
QY 22 VICNVGKWRRLARLQKVDSTKIDSDIEDYPRNLTFRVRESRIWKNTKENTATVAHLV 81  
DB 1405 VIREHLGLSMAELARELQFVSVDINRIRVENPNSLDQSTALLTLWVDREGENAKMENLY 1464  
QY 82 GALSRCQNLVADIVQ-EVQARDLQ-----NRSGAMSP 114  
DB 1465 TALNRIDRSEIVNLEGGQSRNLKPERRHGRDREYSLSP 1504  
RESULT 8  
T09479  
serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09479; I38992  
R;Huang, J.; Hsu, H.B.; Baichwal, V.R.; Goeddel, D.V.  
submitted to the EMBL Data Library, August 1998  
A;Reference number: Z16685  
A;Accession: T09479  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-671 <HUA>  
A;Cross-references: UNIPROT:Q13546; EMBL:U50062; NID:g3426026; PID:g3426027  
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A;Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (CD95)  
A;Reference number: A56913; MUID:95277838; PMID:7538908  
A;Accession: I38992  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 300-513 <RES>  
A;Cross-references: EMBL:U25994; NID:g829616; PIDN:AAC50137.1; PID:g829617

C;Genetics:  
A;Gene: RIP  
C;Keywords: ATP binding; phosphotransferase  
Query Match 18.8%; Score 111.5; DB 2; Length 671;  
Best Local Similarity 36.4%; Pred. No. 0.0096;  
Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;  
QY 23 ICNVGKWRRLARLQKVDSTKIDSDIEDYPRNLTFRVRESRIWKNTK-ENATVAHL 80  
DB 590 IRENGLKHWKNCARKLGTQSQIDEIDHVDYERDGLKEKVYQMLQKWYMRGKIGATVGL 649  
QY 81 VGALRSC-OMNLVADIV 96  
DB 650 AQALHOCSDILLUSLI 666  
RESULT 9  
T15347  
ankyrin-related unc-44 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282  
R;Gattung, S.  
submitted to the EMBL Data Library, February 1996  
A;Description: The sequence of C. elegans cosmid B0350.  
A;Reference number: Z18332  
A;Accession: T15347  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2039 <GAT>  
A;Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA934  
A;Accession: T15346  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVA  
32, 'S', 2034-2035, 'GSPTRSVPEHRHSQEDHEGST' <GA2>  
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1  
A;Accession: T15344  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAEISTEQVPE', 1934-1935, 'E  
<GA3>  
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1  
A;Accession: T15345  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE  
PTRSVPEHRHSQEDHEGST' <GA4>  
R;Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoo  
J. Cell Biol. 129, 1081-1092, 1995  
A;Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae  
A;Reference number: A57282; MUID:95263663; PMID:7744957  
A;Accession: A57282  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-852, 'GGG', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE  
, 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHS' <OTS>  
A;Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608  
A;Accession: B57282  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E  
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'STRRSVPEHRHS', 1984-1985, 'EDHEGS', 'E  
A;Cross-references: GB:U21731  
A;Accession: C57282  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'O', 414, 824, 'S', 826, 'ER', 829, 'E  
4, 'TIV', 1828, 'ESTS', 1833, 'OV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVT', 194  
A;Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604  
C;Genetics:

A;Gene: CESP:unc-44  
A;Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979/2  
C;Superfamily: ankyrin; ankyrin repeat homology  
F;164-192/Domain: ankyrin repeat homology <AN04>  
F;358-390/Domain: ankyrin repeat homology <AN1>  
F;391-423/Domain: ankyrin repeat homology <AN11>  
Query Match 17.4%; Score 103; DB 2; Length 2039;  
Best Local Similarity 31.9%; Pred. No. 0.21; Mismatches 15; Gaps 3;  
Matches 30; Conservative 15; Indels 41; Gaps 8; Gaps 3;  
QY 23 ICDNVGKWRRLARLQKVSDDTKIDSDYPRNLTVRESRIWKTEKENATVAHLVG 82  
Db 1504 VLKIGADWPRGLAEVPHDIHQIRQYPP--GQECKNTLKIWIHLKKEDANQDNLQ 1560  
QY 83 ALRSCQMLVADLVQVEQVQARD--LQNRSGMSP 114  
Db 1561 ALRQIGRD---DIVRSIAYGEPDALINYQADSP 1591  
RESULT 10  
S37431  
ankyrin 2, neuronal long splice form - human  
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid  
N;Contains: ankyrin 2, short form  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569  
R;Chan, W.  
submitted to the EMBL Data Library, September 1993  
A;Reference number: S37431  
A;Accession: S37431  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-3924 <CHA>  
A;Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406287  
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a  
A;Reference number: A39643; MUID:91302466; PMID:1830053  
A;Accession: A39643  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2077 <OT1>  
A;Cross-references: GB:X56957  
A;Accession: B39643  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1443, 3585-3924 <OTT>  
A;Cross-references: EMBL:X56958  
R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,  
Genomics 10, 858-866, 1991  
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A;Reference number: A40334; MUID:92009921; PMID:1833308  
A;Accession: A40334  
A;Molecule type: DNA  
A;Residues: 463-474, PE, 477-495 <TSE>  
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
R;Chan, W.; Kordeli, E.; Bennett, V.  
J. Cell Biol. 123, 1463-1473, 1993  
A;Title: 440-KD ankyrinB: structure of the major developmentally regulated domain and se  
A;Accession: A49462  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-3924 <RES>  
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
C;Genetics:  
A;Gene: GDB:ANK2  
A;Cross-references: GDB:127607; OMIM:106410  
A;Map position: 4q25-4q27  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing

F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>  
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>  
F;63-95/Domain: ankyrin repeat homology <AN01>  
F;96-128/Domain: ankyrin repeat homology <AN02>  
F;129-161/Domain: ankyrin repeat homology <AN03>  
F;162-190/Domain: ankyrin repeat homology <AN04>  
F;191-223/Domain: ankyrin repeat homology <AN05>  
F;232-264/Domain: ankyrin repeat homology <AN06>  
F;265-297/Domain: ankyrin repeat homology <AN07>  
F;298-330/Domain: ankyrin repeat homology <AN08>  
F;331-363/Domain: ankyrin repeat homology <AN09>  
F;364-396/Domain: ankyrin repeat homology <AN10>  
F;397-429/Domain: ankyrin repeat homology <AN11>  
F;430-462/Domain: ankyrin repeat homology <AN12>  
F;463-495/Domain: ankyrin repeat homology <AN13>  
F;496-528/Domain: ankyrin repeat homology <AN14>  
F;529-561/Domain: ankyrin repeat homology <AN15>  
F;562-594/Domain: ankyrin repeat homology <AN16>  
F;595-627/Domain: ankyrin repeat homology <AN17>  
F;628-660/Domain: ankyrin repeat homology <AN18>  
F;661-693/Domain: ankyrin repeat homology <AN19>  
F;694-726/Domain: ankyrin repeat homology <AN20>  
F;727-759/Domain: ankyrin repeat homology <AN21>  
F;760-792/Domain: ankyrin repeat homology <AN22>  
F;793-825/Domain: ankyrin repeat homology <AN23>  
Query Match 16.3%; Score 96.5; DB 2; Length 3924;  
Best Local Similarity 24.3%; Pred. No. 1.8; Mismatches 21; Indels 15; Gaps 1;  
Matches 25; Conservative 21; Mismatches 42; Indels 15; Gaps 1;  
QY 23 ICDNVGKWRRLARLQKVSDDTKIDSDYPRNLTVRESRIWKTEKENATVAHLVG 82  
Db 3543 IADHLGFWSTELARELDFTTEQIHQIRIENPNLSQDSQYLLKIMLWDGKHATDTNLVE 3602  
QY 83 ALRSCQMLVADLVQ-----EVQARDLQNRSG 110  
Db 3603 CLTKINRMDIVHLMETNTPELQERISHVAEIEQTITLDHSEG 3645  
RESULT 11  
JC2395  
Fas antigen precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: JC2395; PC2246  
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liv  
A;Reference number: JC2395; MUID:94128114; PMID:7507668  
A;Accession: JC2395  
A;Molecule type: mRNA  
A;Residues: 1-324 <KIM>  
A;Cross-references: UNIPROT:Q63199; DBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d100  
A;Experimental source: thymus  
A;Accession: PC2246  
A;Molecule type: mRNA  
A;Residues: 1-62, 'RPT', <K12>  
A;Cross-references: DBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g46848  
A;Experimental source: liver  
C;Genetics:  
A;Introns: 62/1  
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homol  
C;Keywords: transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-324/Product: Fas antigen #status predicted <MAT>  
F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>  
F;171-188/Domain: transmembrane #status predicted <TMW>  
Query Match 15.7%; Score 93; DB 2; Length 324;  
Best Local Similarity 28.2%; Pred. No. 0.24; Mismatches 16; Indels 8; Gaps 2;  
Matches 22; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

A;Reference number: A45526; MUID:89314048; PMID:2664506  
A;Accession: B45526  
A;Status: preliminary  
A;Molecule type: DNA

A:Residues: 'R',1491-1556 <WE2>  
A:Cross-references: GB:J04645  
A>Note: the authors translated the codon TTG for residue 1540 as Lys  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP; nucleotide binding; P-loop  
F:89-773/Domain: myosin motor domain homology <MMOT>  
F:179-186/Region: nucleotide-binding motif A (P-loop)  
  
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Best Local Similarity 28.0%; Pred. No. 8.3; 32; Indels 12; Gaps 4;  
Matches 26; Conservative 23; Mismatches 32; Indels 12; Gaps 4;  
  
QY 25 DNVGKDWRLAROLKYSYDTKIDISIE---DRYPNLTERTVRESLRIRWKTEKENATVAHLV 81  
DB 1053 NEIEKQKRGKIGGLKVAQENMEEIERQHEIESNLAKKGESEAQAITTRLEEQ----DLL 1108  
  
QY 82 GALRSQ---MNLVADLVQEVQOARDLQNRSGA 111  
DB 1109 GSLKTCQRTTQNRRISELELENER--QSRKA 1139

Search completed: February 11, 2005, 16:41:35  
Job time : 67 secs

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